

## SEQUENCE LISTING

<110> Lukyanov, Sergey

<120> FLUORESCENT PROTEINS FROM COPEPODA SPECIES AND METHODS FOR USING SAME

<130> U 015759-8

<140> 10/533,781

<141> 2005-05-04

<160> 28

<170> PatentIn version 3.1

<210> 1

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<212> DNA

<213> *Pontellina plumata*

<400> 1

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<212> PRT

<213> *Pontellina plumata*

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                   20                    25                    30  
 Arg Met Thr Asn Lys Met Lys Ser Thr Lys Gly Ala Leu Thr Phe Ser  
                   35                    40                    45  
 Pro Tyr Leu Leu Ser His Val Met Gly Tyr Gly Phe Tyr His Phe Gly  
                   50                    55                    60  
 Thr Tyr Pro Ser Gly Tyr Glu Asn Pro Phe Leu His Ala Ala Asn Asn  
 65                    70                    75                    80  
 Gly Gly Tyr Thr Asn Thr Arg Ile Glu Lys Tyr Glu Asp Gly Gly Val  
                   85                    90                    95  
 Leu His Val Ser Phe Ser Tyr Arg Tyr Glu Ala Gly Arg Val Ile Gly  
                   100                    105                    110  
 Asp Phe Lys Val Val Gly Thr Gly Phe Pro Glu Asp Ser Val Ile Phe  
                   115                    120                    125  
 Thr Asp Lys Ile Ile Arg Ser Asn Ala Thr Val Glu His Leu His Pro  
                   130                    135                    140  
 Met Gly Asp Asn Val Leu Val Gly Ser Phe Ala Arg Thr Phe Ser Leu  
 145                    150                    155                    160  
 Arg Asp Gly Gly Tyr Tyr Ser Phe Val Val Asp Ser His Met His Phe  
                   165                    170                    175  
 Lys Ser Ala Ile His Pro Ser Ile Leu Gln Asn Gly Gly Ser Met Phe  
                   180                    185                    190  
 Ala Phe Arg Arg Val Glu Glu Leu His Ser Asn Thr Glu Leu Gly Ile  
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<212> DNA

<213> Pontellina plumata

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 ctctgagca gggacgtatg accaacaaga tgaagtctac caagggcgcc ttgaccttct      180  
 cccctacct tctctctcat gtcatgggat acgggttcta ccactttggt acctatccca      240  
 gtgggtatga gaatcccttc ctgcatgccca tcaacaacgg ggggtacacc aacaccagga      300

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tcaccgacaa gatcatccgg tccaatgcta ccgtggagca cttgcaccca atgggagaca      480
acgttcttgtt gggctccttc gcgagaacct tttccctgag ggatggaggc tactactcat      540
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ggggggcccat gtttgccttc aggagagttg aggaacttca ctccaacact gaacttggca      660
ttgtagagta tcaacatgcc ttcaagactc ccatagcatt tgcttaaact acaaagtatc      720
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atccttgttg ctctgttgat atgaacactt tctgacttgg accccggctt gaactgaccc      900
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<213> Pontellina plumata

<400> 4

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          20           25           30
Arg Met Thr Asn Lys Met Lys Ser Thr Lys Gly Ala Leu Thr Phe Ser
          35           40           45
Pro Tyr Leu Leu Ser His Val Met Gly Tyr Gly Phe Tyr His Phe Gly
          50           55           60
Thr Tyr Pro Ser Gly Tyr Glu Asn Pro Phe Leu His Ala Ile Asn Asn
65           70           75           80
Gly Gly Tyr Thr Asn Thr Arg Ile Glu Lys Tyr Glu Asp Gly Gly Val
          85           90           95
Leu His Val Ser Phe Ser Tyr Arg Tyr Glu Ala Gly Arg Val Ile Gly
          100          105          110
Asp Phe Lys Val Val Gly Thr Gly Phe Pro Glu Asp Ser Val Ile Phe
          115          120          125
Thr Asp Lys Ile Ile Arg Ser Asn Ala Thr Val Glu His Leu His Pro
          130          135          140
Met Gly Asp Asn Val Leu Val Gly Ser Phe Ala Arg Thr Phe Ser Leu
145          150          155          160
Arg Asp Gly Gly Tyr Tyr Ser Phe Val Val Asp Ser His Met His Phe
          165          170          175

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Lys Ser Ala Ile His Pro Ser Ile Leu Gln Asn Gly Gly Pro Met Phe  
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 Ala Phe Arg Arg Val Glu Glu Leu His Ser Asn Thr Glu Leu Gly Ile  
 195 200 205  
 Val Glu Tyr Gln His Ala Phe Lys Thr Pro Ile Ala Phe Ala  
 210 215 220

<210> 5  
 <211> 814  
 <212> DNA  
 <213> Labidocera aestiva  
 <400> 5

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 gatggaaaca ctgatgaagg acgtatgacc aacaagatga agtccaccaa aggacctctc 180  
 tccttctctc cctacctact ctccacatc atgggctacg gattctatca ctatgctacc 240  
 ttccctgctg gatatgagaa tgtctacctc catgctgcta agaattggagg ctacaccaac 300  
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 gagggaaaca aggttatcgg agacttcaag gttgttgat caggattccc agctaacagt 420  
 gttatcttca ctgacaagat catcaagtcc aaccaaacct gtgagcacat ctaccccaag 480  
 ggagataata ttcttgtcaa tgcctacact cgaacttgga tgctgagaga tgggtggatac 540  
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 cagaacggag gatccatggt tacctacagg aagggtgagg agctccacag ccagtcagat 660  
 gttggtattg tagaatacca acatgtcttc aagaccccaa ctgcttttgc ctaagcttgg 720  
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Met Pro Val Met Lys Ile Glu Cys Arg Ile Ser Gly Thr Met Asn Gly  
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 20 25 30  
 Arg Met Thr Asn Lys Met Lys Ser Thr Lys Gly Pro Leu Ser Phe Ser  
 35 40 45

Pro Tyr Leu Leu Ser His Ile Met Gly Tyr Gly Phe Tyr His Tyr Ala  
 50 55 60  
 Thr Phe Pro Ala Gly Tyr Glu Asn Val Tyr Leu His Ala Ala Lys Asn  
 65 70 75 80  
 Gly Gly Tyr Thr Asn Thr Arg Thr Glu Arg Tyr Glu Asp Gly Gly Ile  
 85 90 95  
 Ile Ser Val Asn Phe Thr Tyr Arg Tyr Glu Gly Asn Lys Val Ile Gly  
 100 105 110  
 Asp Phe Lys Val Val Gly Ser Gly Phe Pro Ala Asn Ser Val Ile Phe  
 115 120 125  
 Thr Asp Lys Ile Ile Lys Ser Asn Pro Thr Cys Glu His Ile Tyr Pro  
 130 135 140  
 Lys Gly Asp Asn Ile Leu Val Asn Ala Tyr Thr Arg Thr Trp Met Leu  
 145 150 155 160  
 Arg Asp Gly Gly Tyr Tyr Ser Ala Gln Val Asn Asn His Leu His Phe  
 165 170 175  
 Lys Thr Ala Met His Pro Thr Met Leu Gln Asn Gly Gly Ser Met Phe  
 180 185 190  
 Thr Tyr Arg Lys Val Glu Glu Leu His Ser Gln Ser Asp Val Gly Ile  
 195 200 205  
 Val Glu Tyr Gln His Val Phe Lys Thr Pro Thr Ala Phe Ala  
 210 215 220

<210> 7

<211> 753

<212> DNA

<213> cf. *Pontella meadi* Wheeler

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 ctccctacct cctctccac attcttggct acggatatta ccactttgca accttccttg 240  
 ctggatatga aaatatctac cttcatgcca tgaagaatgg aggttactcc aatgtcagaa 300  
 ctgagaggta tgaggatgga ggcattcatt ctataacctt caactacaga tatgaaggga 360  
 acaagatcat tggagacttc aagggttggtg gaacaggatt ccctaccaac agtcttatct 420  
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 cccagggttaa caaccatatt cacttcaaga gtgccatcca taccaccatg ctccagaatg 600  
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			20					25					30		
Arg	Met	Thr	Asn	Lys	Met	Lys	Ser	Ile	Lys	Gly	Pro	Ile	Ser	Phe	Ser
		35					40					45			
Pro	Tyr	Leu	Leu	Ser	His	Ile	Leu	Gly	Tyr	Gly	Tyr	Tyr	His	Phe	Ala
	50					55				60					
Thr	Phe	Pro	Ala	Gly	Tyr	Glu	Asn	Ile	Tyr	Leu	His	Ala	Met	Lys	Asn
65				70					75					80	
Gly	Gly	Tyr	Ser	Asn	Val	Arg	Thr	Glu	Arg	Tyr	Glu	Asp	Gly	Gly	Ile
			85					90					95		
Ile	Ser	Ile	Thr	Phe	Asn	Tyr	Arg	Tyr	Glu	Gly	Asn	Lys	Ile	Ile	Gly
		100					105					110			
Asp	Phe	Lys	Val	Val	Gly	Thr	Gly	Phe	Pro	Thr	Asn	Ser	Leu	Ile	Phe
	115					120					125				
Thr	Asp	Lys	Ile	Ile	Lys	Ser	Asn	Pro	Thr	Cys	Glu	Asn	Met	Phe	Pro
	130					135					140				
Lys	Ala	Asp	Asn	Thr	Leu	Val	Asn	Ala	Tyr	Thr	Arg	Thr	Tyr	Leu	Leu
145				150						155				160	
Lys	Asp	Gly	Gly	Tyr	Tyr	Ser	Ala	Gln	Val	Asn	Asn	His	Met	His	Phe
		165						170					175		
Lys	Ser	Ala	Ile	His	Thr	Thr	Met	Leu	Gln	Asn	Gly	Gly	Ser	Met	Phe
		180					185					190			
Thr	Tyr	Arg	Val	Val	Glu	Glu	Thr	His	Thr	Gln	Asn	Glu	Val	Ala	Ile
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	210					215					220				

<210>	9
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<212>	DNA

<213> cf. Pontella meadi Wheeler

<400> 9

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tcaaaatgcc tgacatgaag cttgagtgcc acatctccgg aaccatgaat ggagaggagt      180
ttgaacttat tggttctgga gatggaaata ctgatcaggg acgcatgaca aacaatatga      240
agtccatcaa aggacctctc tccttctctc cctacctact ctcccacatt cttggctatg      300
gatattacca ctttgcaacc ttccctgctg gatatgaaaa tatctacctt catgccatga      360
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taaccttcaa ctacagatat gaaggcagca agatcattgg agacttcaaa gttattggaa      480
caggattccc taccgacagt cttatcttca ctgacaagat cattaaatcc aaccctacct      540
gcgagaacat gttccccaag gctgacaaca ttcttgtgaa tgcctacacc agaacctatt      600
tgcttaaaga tgggtggatac tactctgccc aggttaacaa ccatatgcac ttcaagagtg      660
ccatccatcc tacaatgctc cagaatggtg gatccatggt cactcacaga gtagtagagg      720
agaaccacac taagaccaac gttgctatcg tagagtacca aaatgtcttc aaaactccta      780
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<210> 10

<211> 222

<212> PRT

<213> cf. Pontella meadi Wheeler

<400> 10

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          20           25           30
Arg Met Thr Asn Asn Met Lys Ser Ile Lys Gly Pro Leu Ser Phe Ser
          35           40           45
Pro Tyr Leu Leu Ser His Ile Leu Gly Tyr Gly Tyr Tyr His Phe Ala
          50           55           60
Thr Phe Pro Ala Gly Tyr Glu Asn Ile Tyr Leu His Ala Met Lys Asn
65           70           75           80
Gly Gly Tyr Ser Asn Val Arg Thr Glu Arg Tyr Glu Asp Gly Gly Ile
          85           90           95
Ile Ser Ile Thr Phe Asn Tyr Arg Tyr Glu Gly Ser Lys Ile Ile Gly
          100          105          110
Asp Phe Lys Val Ile Gly Thr Gly Phe Pro Thr Asp Ser Leu Ile Phe
          115          120          125

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Thr	Asp	Lys	Ile	Ile	Lys	Ser	Asn	Pro	Thr	Cys	Glu	Asn	Met	Phe	Pro
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Lys	Ala	Asp	Asn	Ile	Leu	Val	Asn	Ala	Tyr	Thr	Arg	Thr	Tyr	Leu	Leu
145					150					155				160	
Lys	Asp	Gly	Gly	Tyr	Tyr	Ser	Ala	Gln	Val	Asn	Asn	His	Met	His	Phe
				165					170					175	
Lys	Ser	Ala	Ile	His	Pro	Thr	Met	Leu	Gln	Asn	Gly	Gly	Ser	Met	Phe
		180					185						190		
Thr	His	Arg	Val	Val	Glu	Glu	Asn	His	Thr	Lys	Thr	Asn	Val	Ala	Ile
	195						200					205			
Val	Glu	Tyr	Gln	Asn	Val	Phe	Lys	Thr	Pro	Thr	Ala	Phe	Ala		
210						215					220				

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 <211> 847  
 <212> DNA  
 <213> *Pontella mediterranea*  
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tttgaacttg	ttggtgctgg	agaaggaaac	actgatgagg	gacgcatgac	caacaagatg	180
aagtccacca	agggacctct	ttccttctct	ccttatttgc	tctcccacgt	tcttggttat	240
ggatactacc	actatgctac	cttccctgct	ggatatgaaa	atgtctacct	ccatgccatg	300
aagaatggag	gttactccaa	cacaagaact	gagagggtatg	aggatggagg	tatcatttct	360
gctaccttca	actacagata	tgaagggaga	cagattcatg	gagacttcaa	ggttgtagga	420
acgggattcc	ctgccgacag	catcatcttc	actgacaaga	tcatcaagtc	caaccctacc	480
tgtgagcaca	tctaccccaa	ggctaacaat	attcttgtga	atgcttacac	cagaacctgg	540
atgcttagag	atggtggata	ctactctgcc	cagggtcaaca	accacatgca	tttacagagt	600
gccattcatc	ccaccatgct	caagaatggt	ggatctatgt	tcacctacag	aaagggttgag	660
gagctccaca	cacaaactga	agtcggtatt	gttgaatacc	agcatgtctt	caagaggcca	720
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Glu	Glu	Phe	Glu	Leu	Val	Gly	Ala	Gly	Glu	Gly	Asn	Thr	Asp	Glu	Gly
			20					25					30		
Arg	Met	Thr	Asn	Lys	Met	Lys	Ser	Thr	Lys	Gly	Pro	Leu	Ser	Phe	Ser
		35					40					45			
Pro	Tyr	Leu	Leu	Ser	His	Val	Leu	Gly	Tyr	Gly	Tyr	Tyr	His	Tyr	Ala
	50					55					60				
Thr	Phe	Pro	Ala	Gly	Tyr	Glu	Asn	Val	Tyr	Leu	His	Ala	Met	Lys	Asn
65				70						75				80	
Gly	Gly	Tyr	Ser	Asn	Thr	Arg	Thr	Glu	Arg	Tyr	Glu	Asp	Gly	Gly	Ile
			85					90						95	
Ile	Ser	Ala	Thr	Phe	Asn	Tyr	Arg	Tyr	Glu	Gly	Arg	Gln	Ile	His	Gly
		100					105						110		
Asp	Phe	Lys	Val	Val	Gly	Thr	Gly	Phe	Pro	Ala	Asp	Ser	Ile	Ile	Phe
		115					120					125			
Thr	Asp	Lys	Ile	Ile	Lys	Ser	Asn	Pro	Thr	Cys	Glu	His	Ile	Tyr	Pro
	130					135						140			
Lys	Ala	Asn	Asn	Ile	Leu	Val	Asn	Ala	Tyr	Thr	Arg	Thr	Trp	Met	Leu
145				150						155					160
Arg	Asp	Gly	Gly	Tyr	Tyr	Ser	Ala	Gln	Val	Asn	Asn	His	Met	His	Leu
			165					170						175	
Gln	Ser	Ala	Ile	His	Pro	Thr	Met	Leu	Lys	Asn	Gly	Gly	Ser	Met	Phe
		180					185						190		
Thr	Tyr	Arg	Lys	Val	Glu	Glu	Leu	His	Thr	Gln	Thr	Glu	Val	Gly	Ile
		195				200						205			
Val	Glu	Tyr	Gln	His	Val	Phe	Lys	Arg	Pro	Thr	Ala	Phe	Ala		
	210					215					220				

<210> 13

<211> 850

<212> DNA

<213> Pontella mediterranea

<400> 13

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tttgaacttg	ttggtgctgg	agatggaaac	actgatgagg	gacgcatgac	caaccagatg	180
aagtccacaa	agggacctct	ctccttctct	ccctacttgc	tctcccacgt	tcttggtctat	240
ggatactacc	actatgctac	cttccctgct	qqatatqaaa	atgtctacct	ccatgccatg	300

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aagaatggag gttactccaa cacaagaact gagaggtatg acgatggagg tatcatttct 360
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actggattcc ctgccgacag catcatcttc actgacaaga tcatcaagtc caaccctacc 480
tgtgagcaca tctaccccaa ggctgacaat attcttgtga atgcctacac cagaacctgg 540
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gccatccatc ccaccatgct ccagaatggg ggatctatgt tcacctacag aaagggttag 660
gagctccaca cacaaactga agttgggtatt gttgagtacc agcatgtttt caagaggccc 720
acagcttttg cttaattttg taaataaaga aagaatttat aatacaatag tgcttttatg 780
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<210> 14
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<212> PRT
<213> Pontella mediterranea
<400> 14

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          20          25          30
Arg Met Thr Asn Gln Met Lys Ser Thr Lys Gly Pro Leu Ser Phe Ser
          35          40          45
Pro Tyr Leu Leu Ser His Val Leu Gly Tyr Gly Tyr Tyr His Tyr Ala
          50          55          60
Thr Phe Pro Ala Gly Tyr Glu Asn Val Tyr Leu His Ala Met Lys Asn
65          70          75          80
Gly Gly Tyr Ser Asn Thr Arg Thr Glu Arg Tyr Asp Asp Gly Gly Ile
          85          90          95
Ile Ser Ala Thr Phe Asn Tyr Arg Tyr Glu Gly Arg Gln Ile His Gly
          100          105          110
Asp Phe Lys Val Val Gly Thr Gly Phe Pro Ala Asp Ser Ile Ile Phe
          115          120          125
Thr Asp Lys Ile Ile Lys Ser Asn Pro Thr Cys Glu His Ile Tyr Pro
          130          135          140
Lys Ala Asp Asn Ile Leu Val Asn Ala Tyr Thr Arg Thr Trp Met Leu
145          150          155          160
Arg Asp Gly Gly Tyr Tyr Ser Ala Gln Val Asn Asn His Met His Phe
          165          170          175
Lys Ser Ala Ile His Pro Thr Met Leu Gln Asn Gly Gly Ser Met Phe
          180          185          190

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Thr Tyr Arg Lys Val Glu Glu Leu His Thr Gln Thr Glu Val Gly Ile  
 195 200 205  
 Val Glu Tyr Gln His Val Phe Lys Arg Pro Thr Ala Phe Ala  
 210 215 220

<210> 15  
 <211> 821  
 <212> DNA  
 <213> Unknown  
 <220>  
 <223> nucleic acid sequence for pdae1GFP from an unidentified  
 Pontellidae species, complete cds  
 <400> 15

atcagtttaa cttctttcag aagacaacta agacctacca acatggcagc catgaagatt 60  
 gagtgcagga tcaactggaac catgaacgga gtggagtttg agctgggttg aggaggagaa 120  
 ggaaatactg atcagggacg tatgaccaac aagatgaaat ctaccaaggg tccactctcc 180  
 ttctctccct atcttctctc tcatgtcatg ggatatggat tctatcattt tggaacattt 240  
 cccagtgggt atgagaatcc ctatgtccac gccatgacga acggtggata taccaacacc 300  
 aggattgaaa gttatgaaga tggaggtggt ctttacctta ctttcaacta cagattggat 360  
 ggaaacaaga ttatcgggga cttcaagtgt gtcggaactg gattccctga ggacagcgtt 420  
 atcttcactg acaagatcat caagtccaac cccaattgtg aacatttcta tccaatggct 480  
 gaaaacatca tgaaaaatgc ctacatgaga actctctccc tcagagatgg tggctactac 540  
 tctggccagg ttaccagcca catccacttc aagaatgcga tccacccatc catccttcat 600  
 aacggcggat ccatgttcac ctacagaaga gttgaggagc tccacactca aactgatctt 660  
 ggaattgttg agtaccagca tgtattcaag actcccactg cttttgcttg aatgccatga 720  
 agatgaaacc tgaacaagat caatctttat ttaccacaat atgtaaattg tttaattgta 780  
 taattctcga gaattcatat aatacataga atttatctta c 821

<210> 16  
 <211> 222  
 <212> PRT  
 <213> Unknown  
 <220>  
 <223> amino acid sequence for pdae1GFP from an unidentified Pontellidae  
 species  
 <400> 16

Met Ala Ala Met Lys Ile Glu Cys Arg Ile Thr Gly Thr Met Asn Gly  
 1 5 10 15  
 Val Glu Phe Glu Leu Val Gly Gly Gly Glu Gly Asn Thr Asp Gln Gly

20	25	30
Arg Met Thr Asn Lys Met Lys Ser Thr Lys Gly Pro Leu Ser Phe Ser		
35	40	45
Pro Tyr Leu Leu Ser His Val Met Gly Tyr Gly Phe Tyr His Phe Gly		
50	55	60
Thr Phe Pro Ser Gly Tyr Glu Asn Pro Tyr Val His Ala Met Thr Asn		
65	70	75
Gly Gly Tyr Thr Asn Thr Arg Ile Glu Ser Tyr Glu Asp Gly Gly Val		
85	90	95
Leu Tyr Leu Thr Phe Asn Tyr Arg Leu Asp Gly Asn Lys Ile Ile Gly		
100	105	110
Asp Phe Lys Cys Val Gly Thr Gly Phe Pro Glu Asp Ser Val Ile Phe		
115	120	125
Thr Asp Lys Ile Ile Lys Ser Asn Pro Asn Cys Glu His Phe Tyr Pro		
130	135	140
Met Ala Glu Asn Ile Met Lys Asn Ala Tyr Met Arg Thr Leu Ser Leu		
145	150	155
Arg Asp Gly Gly Tyr Tyr Ser Gly Gln Val Thr Ser His Ile His Phe		
165	170	175
Lys Asn Ala Ile His Pro Ser Ile Leu His Asn Gly Gly Ser Met Phe		
180	185	190
Thr Tyr Arg Arg Val Glu Glu Leu His Thr Gln Thr Asp Leu Gly Ile		
195	200	205
Val Glu Tyr Gln His Val Phe Lys Thr Pro Thr Ala Phe Ala		
210	215	220

&lt;210&gt; 17

&lt;211&gt; 669

&lt;212&gt; DNA

&lt;213&gt; Artificial sequence

&lt;220&gt;

&lt;223&gt; nucleic acid sequence for the humanized version of the ppluGFP2

&lt;400&gt; 17

atgcccccca tgaagatcga gtgccgcac accggcaccc tgaacggcgt ggagttcgag	60
ctggtgggcg gcggagaggg ccccccgag cagggccgca tgaccaacaa gatgaagagc	120
accaagggcg ccctgacctt cagcccctac ctgctgagcc acgtgatggg ctacggcttc	180
taccacttcg gcacctacc cagcggctac gagaaccct tcctgcacgc catcaacaac	240
ggcggctaca ccaacacccg catcgagaag tacgaggacg gcggcgtgct gcacgtgagc	300
ttcagctacc gctacgaggc cggccgcgtg atcggcgact tcaaggtggt gggcaccggc	360
ttccccgagg acagcgtgat cttcacgcac aagatcatcc gcagcaacgc caccgtggag	420

```

cacctgcacc ccatgggcga taacgtgctg gtgggcagct tcgcccgcac cttcagcctg      480
cgcgacggcg gctactacag cttcgtggtg gacagccaca tgcacttcaa gagcgccatc      540
caccccagca tcctgcagaa cggggggcccc atgttcgcct tccgccgcgt ggaggagctg      600
cacagcaaca ccgagctggg catcgtggag taccagcacg ccttcaagac cccgatcgca      660
ttcgccctga                                                                669

```

<210> 18

<211> 222

<212> PRT

<213> Artificial sequence

<220>

<223> amino acid sequence for the humanized version of the ppluGFP2

<400> 18

```

Met Pro Ala Met Lys Ile Glu Cys Arg Ile Thr Gly Thr Leu Asn Gly
1           5           10           15
Val Glu Phe Glu Leu Val Gly Gly Gly Glu Gly Thr Pro Glu Gln Gly
          20           25           30
Arg Met Thr Asn Lys Met Lys Ser Thr Lys Gly Ala Leu Thr Phe Ser
          35           40           45
Pro Tyr Leu Leu Ser His Val Met Gly Tyr Gly Phe Tyr His Phe Gly
          50           55           60
Thr Tyr Pro Ser Gly Tyr Glu Asn Pro Phe Leu His Ala Ile Asn Asn
65           70           75           80
Gly Gly Tyr Thr Asn Thr Arg Ile Glu Lys Tyr Glu Asp Gly Gly Val
          85           90           95
Leu His Val Ser Phe Ser Tyr Arg Tyr Glu Ala Gly Arg Val Ile Gly
          100          105          110
Asp Phe Lys Val Val Gly Thr Gly Phe Pro Glu Asp Ser Val Ile Phe
          115          120          125
Thr Asp Lys Ile Ile Arg Ser Asn Ala Thr Val Glu His Leu His Pro
          130          135          140
Met Gly Asp Asn Val Leu Val Gly Ser Phe Ala Arg Thr Phe Ser Leu
145          150          155          160
Arg Asp Gly Gly Tyr Tyr Ser Phe Val Val Asp Ser His Met His Phe
          165          170          175
Lys Ser Ala Ile His Pro Ser Ile Leu Gln Asn Gly Gly Pro Met Phe
          180          185          190
Ala Phe Arg Arg Val Glu Glu Leu His Ser Asn Thr Glu Leu Gly Ile
          195          200          205
Val Glu Tyr Gln His Ala Phe Lys Thr Pro Ile Ala Phe Ala
          210          215          220

```

<210> 19  
 <211> 589  
 <212> DNA  
 <213> Artificial sequence  
 <220>  
 <223> nucleic acid sequence for the ppluGFP2 with yeast-optimized codon usage  
 <400> 19

```

tactccagaa caaggtagaa tgactaataa aatgaaatct actaaagggtg ctttgacttt      60
ttctccatat ttgttgtctc atgttatggg ttatgggttt tatcattttg gtacttatcc      120
atctgggttat gaaaatccat ttttgcattg tattaataat ggtgggttata ctaatactag      180
aattgaaaaa tatgaagatg gtggtgtttt gcatgtttct ttttcttata gatatgaagc      240
tggtagagtt attggcgatt ttaaagttgt tggtactggg tttccagaag attctgttat      300
ttttactgat aaaattatta gatctaatac tactgttgaa catttgcatt caatgggtga      360
taatgttttg gttgggtctt ttgctagaac tttttctttg agagatgggtg gttattattc      420
ttttgttggt gattctcata tgcattttta atctgctatt catccatcta ttttgcaaaa      480
tggtgggtcca atgtttgctt ttagaagagt tgaagaattg cattctaata ctgaattggg      540
tattgttgaa tatcaacatg cttttaaaac tccaattgct tttgcttaa      589
  
```

<210> 20  
 <211> 222  
 <212> PRT  
 <213> Artificial sequence  
 <220>  
 <223> amino acid sequence for the ppluGFP2 with yeast-optimized codon usage  
 <400> 20

```

Met Pro Ala Met Lys Ile Glu Cys Arg Ile Thr Gly Thr Leu Asn Gly
1           5           10           15
Val Glu Phe Glu Leu Val Gly Gly Gly Glu Gly Thr Pro Glu Gln Gly
           20           25           30
Arg Met Thr Asn Lys Met Lys Ser Thr Lys Gly Ala Leu Thr Phe Ser
           35           40           45
Pro Tyr Leu Leu Ser His Val Met Gly Tyr Gly Phe Tyr His Phe Gly
           50           55           60
Thr Tyr Pro Ser Gly Tyr Glu Asn Pro Phe Leu His Ala Ile Asn Asn
65           70           75           80
Gly Gly Tyr Thr Asn Thr Arg Ile Glu Lys Tyr Glu Asp Gly Gly Val
  
```

	85		90		95
Leu His Val Ser Phe Ser Tyr Arg Tyr Glu Ala Gly Arg Val Ile Gly					
	100		105		110
Asp Phe Lys Val Val Gly Thr Gly Phe Pro Glu Asp Ser Val Ile Phe					
	115		120		125
Thr Asp Lys Ile Ile Arg Ser Asn Ala Thr Val Glu His Leu His Pro					
	130		135		140
Met Gly Asp Asn Val Leu Val Gly Ser Phe Ala Arg Thr Phe Ser Leu					
	145		150		155
Arg Asp Gly Gly Tyr Tyr Ser Phe Val Val Asp Ser His Met His Phe					
	165		170		175
Lys Ser Ala Ile His Pro Ser Ile Leu Gln Asn Gly Gly Pro Met Phe					
	180		185		190
Ala Phe Arg Arg Val Glu Glu Leu His Ser Asn Thr Glu Leu Gly Ile					
	195		200		205
Val Glu Tyr Gln His Ala Phe Lys Thr Pro Ile Ala Phe Ala					
	210		215		220

&lt;210&gt; 21

&lt;211&gt; 669

&lt;212&gt; DNA

&lt;213&gt; Artificial sequence

&lt;220&gt;

&lt;223&gt; nucleic acid sequence for the CopCFP mutant

&lt;400&gt; 21

```

atgcccgcca tgaagatcga gtgccgcac accggcaccc tgaacggcgt ggagttcgag      60
ctggtggggc gcgagagagg caccgccgag cagggccgca tgaccaacaa gatgaagagc      120
accaaaggcg ccttgacctt cagcccctac ctgctgagcc acgtgatggg ctggggcttt      180
taccacttcg gcacctacc cagcggctac gagaaccctt tcctgcacgc catcaacaac      240
ggcgggtaca ccaacacccg catcgagaag tacgaggacg gcggcgtgct gcacgtgagc      300
ttcagctacc gctacgaggc cggccgcgtg atcggcgact tcaaggtggt gggcaccggc      360
ttccccgagg acagcgtgat cttcaccgac aagatcatcc gcagcaacgc caccgtggag      420
cacctgcgcc ccatggggcg taacgtgctg gtgggcagct tcgcccgcac cttcagcctg      480
cgcgacggcg gctactacag cttcgtggtg gacagccaca tgcacttcaa gagcgccatc      540
caccacagca tcctgcagaa cgggggcccc atgttcgcct tccgccgcgt ggaggagctg      600
cacagcaaca ccgagctggg catcgtggag taccagcacg ccttcaagac cccgaccgca      660
ttcgctaa

```

&lt;210&gt; 22

&lt;211&gt; 222

<212> PRT

<213> Artificial sequence

<220>

<223> amino acid sequence for the CopCFP mutant

<400> 22

```

Met Pro Ala Met Lys Ile Glu Cys Arg Ile Thr Gly Thr Leu Asn Gly
1           5           10           15
Val Glu Phe Glu Leu Val Gly Gly Gly Glu Gly Thr Pro Glu Gln Gly
          20           25           30
Arg Met Thr Asn Lys Met Lys Ser Thr Lys Gly Ala Leu Thr Phe Ser
          35           40           45
Pro Tyr Leu Leu Ser His Val Met Gly Trp Gly Phe Tyr His Phe Gly
          50           55           60
Thr Tyr Pro Ser Gly Tyr Glu Asn Pro Phe Leu His Ala Ile Asn Asn
65           70           75           80
Gly Gly Tyr Thr Asn Thr Arg Ile Glu Lys Tyr Glu Asp Gly Gly Val
          85           90           95
Leu His Val Ser Phe Ser Tyr Arg Tyr Glu Ala Gly Arg Val Ile Gly
          100          105          110
Asp Phe Lys Val Val Gly Thr Gly Phe Pro Glu Asp Ser Val Ile Phe
          115          120          125
Thr Asp Lys Ile Ile Arg Ser Asn Ala Thr Val Glu His Leu Arg Pro
          130          135          140
Met Gly Asp Asn Val Leu Val Gly Ser Phe Ala Arg Thr Phe Ser Leu
145          150          155          160
Arg Asp Gly Gly Tyr Tyr Ser Phe Val Val Asp Ser His Met His Phe
          165          170          175
Lys Ser Ala Ile His Pro Ser Ile Leu Gln Asn Gly Gly Pro Met Phe
          180          185          190
Ala Phe Arg Arg Val Glu Glu Leu His Ser Asn Thr Glu Leu Gly Ile
          195          200          205
Val Glu Tyr Gln His Ala Phe Lys Thr Pro Thr Ala Phe Ala
          210          215          220

```

<210> 23

<211> 690

<212> DNA

<213> Artificial sequence

<220>

<223> nucleic acid sequence for the CopGFP-NA1 variant

<400> 23



```

atggagagcg acgagagcgg cctgcccgcc atggagatcg agtgccgcat caccggcacc      60
ctgaacggcg tggagttcga gctggtgggc ggcggagagg gcacccccga gcagggccgc      120
atgaccaaca agatgaagag caccaagggc gccctgacct tcagccccta cctgctgagc      180
cacgtgatgg gctacggctt ctaccacttc ggcacctacc ccagcggcta cgagaacccc      240
ttcctgcacg ccatcaacaa cggcgggtac accaacaccc gcatcgagaa gtacgaggac      300
ggcggcggtg tgcacgtgag cttcagctac cgctacgagg ccggccgcgt gatcggcgac      360
ttcaagggtg tgggcaccgg cttccccgag gacagcgtga tcttcaccga caagatcatc      420
cgcagcaacg ccaccgtgga gcacctgcac cccatgggcg ataacgtgct ggtgggcagc      480
ttcgcccgca ccttcagcct gcgcgacggc ggctactaca gcttcgtggt ggacagccac      540
atgcacttca agagcgccat ccaccccagc atcctgcaga acggggggccc catgttcgcc      600
ttccgccgcg tggaggagct gcacagcaac accgagctgg gcatcgtgga gtaccagcac      660
gccttcaaga ccccgatcgc attcgctga                                     690

```

<210> 24

<211> 229

<212> PRT

<213> Artificial sequence

<220>

<223> amino acid sequence for the CopGFP-NA1 variant

<400> 24

```

Met Glu Ser Asp Glu Ser Gly Leu Pro Ala Met Glu Ile Glu Cys Arg
1              5              10              15
Ile Thr Gly Thr Leu Asn Gly Val Glu Phe Glu Leu Val Gly Gly Gly
              20              25              30
Glu Gly Thr Pro Glu Gln Gly Arg Met Thr Asn Lys Met Lys Ser Thr
              35              40              45
Lys Gly Ala Leu Thr Phe Ser Pro Tyr Leu Leu Ser His Val Met Gly
              50              55              60
Tyr Gly Phe Tyr His Phe Gly Thr Tyr Pro Ser Gly Tyr Glu Asn Pro
65              70              75              80
Phe Leu His Ala Ile Asn Asn Gly Gly Tyr Thr Asn Thr Arg Ile Glu
              85              90              95
Lys Tyr Glu Asp Gly Gly Val Leu His Val Ser Phe Ser Tyr Arg Tyr
              100             105             110
Glu Ala Gly Arg Val Ile Gly Asp Phe Lys Val Val Gly Thr Gly Phe
              115             120             125
Pro Glu Asp Ser Val Ile Phe Thr Asp Lys Ile Ile Arg Ser Asn Ala
              130             135             140
Thr Val Glu His Leu His Pro Met Gly Asp Asn Val Leu Val Gly Ser

```

145	150	155	160
Phe Ala Arg Thr Phe Ser Leu Arg Asp Gly Gly Tyr Tyr Ser Phe Val			
	165	170	175
Val Asp Ser His Met His Phe Lys Ser Ala Ile His Pro Ser Ile Leu			
	180	185	190
Gln Asn Gly Gly Pro Met Phe Ala Phe Arg Arg Val Glu Glu Leu His			
	195	200	205
Ser Asn Thr Glu Leu Gly Ile Val Glu Tyr Gln His Ala Phe Lys Thr			
210	215	220	

Pro Ile Ala Phe Ala

225

<210> 25

<211> 819

<212> DNA

<213> Artificial sequence

<220>

<223> nucleic acid sequence for the CopGFP-NA2 variant

<400> 25

atgcccgcga tgaagatcga gtgccgcac accggcaccc tgaacggcgt ggagttcgag	60
ctggtggggcg gcggagaggg ccccccgag cagggccgca tgaccaacaa gatgaagagc	120
accaagggcg ccctgacctt cagcccctac ctgctgagcc acgtgatggg ctacggcttc	180
taccacttcg gcacctacc cagcggctac gagaaccctt tcctgcacgc catcaacaac	240
ggcggctaca ccaacacccg catcgagaag tacgaggacg gcggcgtgct gcacgtgagc	300
ttcagctacc gctacgaggc cggccgcgtg atcggcgact tcaaggtggt gggcaccggc	360
ttccccgagg acagcgtgat cttcaccgac aagatcatcc gcagcaacgc caccgtggag	420
cacctgcacc ccatgggcca taacgtgctg gtgggcagct tcgcccgcac cttcagcctg	480
cgcgacggcg gctactacag cttcgtggtg gacagccaca tgcacttcaa gagcgccatc	540
caccccagca tcctgcagaa cgggggcccc atgttcgcct tcgcccgcgt ggaggagctg	600
cacagcaaca ccgagctggg catcgtggag taccagcacg ccttcaagac cccgatcgca	660
ttcgccagat ccagagccca ggccagcaac tccgccgtgg atggcacagc cggaccggga	720
tcggccgcga ctctagatca taatcagcca taccacattt gtagaggttt tacttgcttt	780
aaaaaacctc ccacacctcc ccctgaacct gaaacataa	819

<210> 26

<211> 272

<212> PRT

<213> Artificial sequence

<220>

<223> amino acid sequence for the CopGFP-NA2 variant

&lt;400&gt; 26

```

Met Pro Ala Met Lys Ile Glu Cys Arg Ile Thr Gly Thr Leu Asn Gly
1           5           10           15

Val Glu Phe Glu Leu Val Gly Gly Gly Glu Gly Thr Pro Glu Gln Gly
          20           25           30
Arg Met Thr Asn Lys Met Lys Ser Thr Lys Gly Ala Leu Thr Phe Ser
          35           40           45
Pro Tyr Leu Leu Ser His Val Met Gly Tyr Gly Phe Tyr His Phe Gly
          50           55           60
Thr Tyr Pro Ser Gly Tyr Glu Asn Pro Phe Leu His Ala Ile Asn Asn
65           70           75           80
Gly Gly Tyr Thr Asn Thr Arg Ile Glu Lys Tyr Glu Asp Gly Gly Val
          85           90           95
Leu His Val Ser Phe Ser Tyr Arg Tyr Glu Ala Gly Arg Val Ile Gly
          100          105          110
Asp Phe Lys Val Val Gly Thr Gly Phe Pro Glu Asp Ser Val Ile Phe
          115          120          125
Thr Asp Lys Ile Ile Arg Ser Asn Ala Thr Val Glu His Leu His Pro
          130          135          140
Met Gly Asp Asn Val Leu Val Gly Ser Phe Ala Arg Thr Phe Ser Leu
145          150          155          160
Arg Asp Gly Gly Tyr Tyr Ser Phe Val Val Asp Ser His Met His Phe
          165          170          175
Lys Ser Ala Ile His Pro Ser Ile Leu Gln Asn Gly Gly Pro Met Phe
          180          185          190
Ala Phe Arg Arg Val Glu Glu Leu His Ser Asn Thr Glu Leu Gly Ile
          195          200          205
Val Glu Tyr Gln His Ala Phe Lys Thr Pro Ile Ala Phe Ala Arg Ser
          210          215          220
Arg Ala Gln Ala Ser Asn Ser Ala Val Asp Gly Thr Ala Gly Pro Gly
225          230          235          240
Ser Ala Ala Thr Leu Asp His Asn Gln Pro Tyr His Ile Cys Arg Gly
          245          250          255
Phe Thr Cys Phe Lys Lys Pro Pro Thr Pro Pro Pro Glu Pro Glu Thr
          260          265          270

```

&lt;210&gt; 27

&lt;211&gt; 840

&lt;212&gt; DNA

<213> Artificial sequence

<220>

<223> nucleic acid sequence for the CopGFP-NA3 variant

<400> 27

```

atggagagcg acgagagcgg cctgcccgcc atggagatcg agtgccgcat caccggcacc      60
ctgaacggcg tggagttcga gctggtgggc ggcggagagg gcacccccga gcagggccgc      120
atgaccaaca agatgaagag caccaagggc gccctgacct tcagccccta cctgctgagc      180
cacgtgatgg gctacggctt ctaccacttc ggcacctacc ccagcggcta cgagaacccc      240
ttcctgcacg ccatcaacaa cggcgggtac accaacaccc gcatcgagaa gtacgaggac      300
ggcggcgctg tgcacgtgag cttcagctac cgctacgagg ccggccgcgt gatcggcgac      360
ttcaaggtgg tgggcaccgg cttccccgag gacagcgtga tcttcaccga caagatcatc      420
cgcagcaacg ccaccgtgga gcacctgcac cccatgggcg ataacgtgct ggtgggcagc      480
ttcgcccgca ccttcagcct gcgcgacggc ggctactaca gcttcgtggt ggacagccac      540
atgcacttca agagcgccat ccaccccagc atcctgcaga acggggggccc catgttcgcc      600
ttccgccgcy tggaggagct gcacagcaac accgagctgg gcatcgtgga gtaccagcac      660
gccttcaaga ccccgatcgc attcgccaga tccagagccc aggccagcaa ctccgccgtg      720
gatggcacag ccggaccggg atcgggccgc actctagatc ataatcagcc ataccacatt      780
tgtagagggt ttacttgctt taaaaaacct cccacacctc cccctgaacc tgaaacataa      840

```

<210> 28

<211> 279

<212> PRT

<213> Artificial sequence

<220>

<223> amino acid sequence for the CopGFP-NA3 variant

<400> 28

```

Met Glu Ser Asp Glu Ser Gly Leu Pro Ala Met Glu Ile Glu Cys Arg
1              5              10              15
Ile Thr Gly Thr Leu Asn Gly Val Glu Phe Glu Leu Val Gly Gly Gly
              20              25              30
Glu Gly Thr Pro Glu Gln Gly Arg Met Thr Asn Lys Met Lys Ser Thr
              35              40              45
Lys Gly Ala Leu Thr Phe Ser Pro Tyr Leu Leu Ser His Val Met Gly
              50              55              60
Tyr Gly Phe Tyr His Phe Gly Thr Tyr Pro Ser Gly Tyr Glu Asn Pro
65              70              75              80
Phe Leu His Ala Ile Asn Asn Gly Gly Tyr Thr Asn Thr Arg Ile Glu
              85              90              95
Lys Tyr Glu Asp Gly Gly Val Leu His Val Ser Phe Ser Tyr Arg Tyr
              100              105              110

```

Glu Ala Gly Arg Val Ile Gly Asp Phe Lys Val Val Gly Thr Gly Phe  
 115 120 125  
 Pro Glu Asp Ser Val Ile Phe Thr Asp Lys Ile Ile Arg Ser Asn Ala  
 130 135 140  
  
 Thr Val Glu His Leu His Pro Met Gly Asp Asn Val Leu Val Gly Ser  
 145 150 155 160  
 Phe Ala Arg Thr Phe Ser Leu Arg Asp Gly Gly Tyr Tyr Ser Phe Val  
 165 170 175  
 Val Asp Ser His Met His Phe Lys Ser Ala Ile His Pro Ser Ile Leu  
 180 185 190  
 Gln Asn Gly Gly Pro Met Phe Ala Phe Arg Arg Val Glu Glu Leu His  
 195 200 205  
 Ser Asn Thr Glu Leu Gly Ile Val Glu Tyr Gln His Ala Phe Lys Thr  
 210 215 220  
 Pro Ile Ala Phe Ala Arg Ser Arg Ala Gln Ala Ser Asn Ser Ala Val  
 225 230 235 240  
 Asp Gly Thr Ala Gly Pro Gly Ser Ala Ala Thr Leu Asp His Asn Gln  
 245 250 255  
 Pro Tyr His Ile Cys Arg Gly Phe Thr Cys Phe Lys Lys Pro Pro Thr  
 260 265 270  
 Pro Pro Pro Glu Pro Glu Thr  
 275